```
FILE 'REGISTRY' ENTERED AT 09:55:[illegible] ON 17 APR 2003

=> S N-ACETYL AMINO ACID RACEMASE OR
L1             2 N-ACETYL AMINO ACID RACEMASE OR

=> S AMINO ACID RACEMASE OR
L2             1 AMINO ACID RACEMASE OR

=> D

L3   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2003 ACS
RN   9164-21-0  REGISTRY
CN   Racemase, amino acid  (8CI)    DA INDEX NAME
OTHER NAMES:
CN     ***Amino acid racemase***
CN   E.C. 5.1.1.10
CN   L-Amino acid racemase
MF   Unspecified
CI   MAN
LC   STN Files:   ADISCTA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CEN, TOXCENTER,
       USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
               84 REFERENCES IN FILE CA (1962 TO DATE)
               84 REFERENCES IN FILE CAPLUS (1962 TO DATE)


FILE 'CAPLUS' ENTERED AT 09:56:38 ON 17 APR 2003

=> S AMINO ACID RACEMASE;S L2;S L3,L4
         914834 AMINO
             42 AMINOS
         914851 AMINO
                (AMINO OR AMINOS)
        3607955 ACID
        1370818 ACIDS
        4069468 ACID
                (ACID OR ACIDS)
           1089 RACEMASE
            143 RACEMASES
           1110 RACEMASE
                (RACEMASE OR RACEMASES)
            110 AMINO ACID RACEMASE
                (AMINO(W)ACID(W)RACEMASE)

L4             84 L2

L5            115 (L3 OR L4)

=> S ANTICHLAMYDIS
L6            435 ANTICHLAMYDIS

=> S L5 AND L6
L7              3 L5 AND L6

=> D 1-3 CBIB ABS

L7   ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2003 ACS
2003:391502   Document No. 136:330962  Method for producing enantiomerically
      enriched amino acids from N-substituted amino acids.  Rommarius, Andreas;
      Turner, Stefan; Drauz, Karlheinz  (Degussa A.-G., Germany).  Eur. Pat.
      Appl.  EP 1179603 A1 20020417, 12 pp.  DESIGNATED STATES:  R:  AT, BE, CH,
      DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI,
      RO.  (German).  CODEN: EPXXDW.  APPLICATION: EP 2001-124429 20011011.
      PRIORITY: DE 2000-10050123 20001011.
AB   A process is provided for the prodn. of enantiomerically enriched amino
      acids.  The envisioned process employs a N-acetyl- ***amino***
        ***acid***     ***racemase***  in conjunction with an amino acid acylase.
```

L7 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS
1996:715613 Document No. 126:11771 An effective production of optically active amino acids. Tokuyama, Shinji; Hatano, Kazunori (Fac. Agric., Shizuoka Univ., Shizuoka, 422, Japan). Baiosaiensu to Indasutori, 54(11), [illegible] (Japanese) 1996. CODEN: [illegible]. ISSN: 0914-8981. Publisher: Baiotekunoroji Kyokai.
AB A review with 7 refs. After the screening of various strains of bacteria, actinomycetes, molds and yeasts, actinomycetes have been found that produce a novel N-acyl ***amino*** ***acid*** ***racemase*** . Among actinomycetes, ***Amycolatopsis*** sp. TS-1-60 strain isolated from soil shows the highest prodn. of N-acyl ***amino*** ***acid*** ***racemase*** . Properties of the enzyme are described. Large-scale prodn. of the enzyme becomes possible by transformation of the N-acylamino acid racemase gene into E. coli. Purified optically active amino acid can be obtained by passing N-aminoacyl DL-amino acid through a column of DEAE-Toyopearl 650 M to which aminoacylase and racemase are bound.

=> S N-CARBAMOYL AMINO ACID
1562614 N
21342 CARBAMOYL
9 CARBAMOYLS
21346 CARBAMOYL
(CARBAMOYL OR CARBAMOYLS)
914334 AMINO
42 AMINOS
914351 AMINO
(AMINO OR AMINOS)
3607955 ACID
1370818 ACIDS
4069468 ACID
(ACID OR ACIDS)
L8 38 N-CARBAMOYL AMINO ACID
(N(W)CARBAMOYL(W)AMINO(W)ACID)

=> S N CARBAMOYL AMINO ACID
1562614 N
21342 CARBAMOYL
9 CARBAMOYLS
21346 CARBAMOYL
(CARBAMOYL OR CARBAMOYLS)
914334 AMINO
42 AMINOS
914351 AMINO
(AMINO OR AMINOS)
3607955 ACID
1370818 ACIDS
4069468 ACID
(ACID OR ACIDS)
L9 38 N CARBAMOYL AMINO ACID
(N(W)CARBAMOYL(W)AMINO(W)ACID)

=> S L9 AND L5
L10 2 L9 AND L5

=> S L10 NOT L7
L11 2 L10 NOT L7

=> D 1-2 IBIB ABS

L11 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS
2000:520535 Document No. 133:252690 Microbial and enzymic synthesis of optically pure D- and L-3-trimethylsilyl-alanine by deracemization of D,L-5-trimethylsilylmethyl-hydantoin. Pietzsch, Markus; Waniek, Thomas; Smith, Richard J.; Bratovanov, Svetoslav; Bienz, Stefan; Syldatk, Christoph (Institute of Biochemical Engineering, University of Stuttgart, Stuttgart, D-70569, Germany). Monatshefte fuer Chemie, 131(6), 645-653 (English) 2000. CODEN: MOCMB7. ISSN: 0026-9247. Publisher: Springer-Verlag Wien.
AB The stereospecificities of hydantoinases and ***N*** - ***carbamoyl*** ***amino*** ***acid*** amidohydrolases (N-carbamoylases) from

synthesis of the unnatural silicon-containing amino acids D- and L-(4-trimethylsilyl)-alanine (I) from the resp. racemic hydantoin, D,L-I. In a preparative biotransformation, whole resting cells of Agrobacterium sp. IP I-671, immobilized in a Ca-alginate matrix, were used for the synthesis of enantiomerically pure L-I in 49% yield and 99% enantiomeric excess. Since the purified L-N-carbamoylase from Agrobacterium sp. IP I-671 was shown to be 100% L-selective, the enantiomeric purity of more than 99% L-I arising from the transformation with the immobilized cells must be explained by the participation of a further, L-selective N-carbamoylase or, which is more likely, by racemization of the final hydrolysis product by the action of an ***amino*** ***acid*** ***racemase*** . Isolated hydantoinases from Bacillus thermoglucosidasius, Thermus sp., Arthrobacter aurescens DSM 3747, and Arthrobacter crystallopoietes DSM 20117 turned out to be stereospecific for the conversion of the D-form of hydantoin D,L-I. The enantiomerically pure L-form of I was also prepd. It was synthesized from racemic ***N*** - ***carbamoyl*** ***amino*** ***acid*** , D,L-I, by enantiomer-specific hydrolysis of the L-form in presence of L-N-carbamoylase from Arthrobacter aurescens DSM 3747.

L11 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS
AN 1998:[illegible]326 Document No. 169:127526 Manufacture of L-.alpha.-amino acids from hydantoins or N-carbamoyl-.alpha.-amino acids with microorganisms or microbial enzymes. Hoelzmann, Wilhelm; Wagner, Fritz; Cotoras, Davor; Syldatk, Christoph; Bombach, Giselher; Gross, Christiane; Gross, Christiane Dipl Biol; Wagner, Thomas (Ruetgerswerke A.-G., Fed. Rep. Ger.). Ger. Offen. DE 19712539 A1 19980211, 6 pp. (German). CODEN: GWXXBX. APPLICATION: DE 1997-19712539 19970413. PRIORITY: DE 1996-19635012 19960724.
AB Microorganisms or exts. therefrom contg. the enzymes hydantoinase-DL-carbamoyl-.alpha.- ***amino*** ***acid*** ***racemase*** and L-N-carbamoyl-.alpha.-amino acid amidohydrolase, are used to prep. L-.alpha.-amino acids from 5-substituted hydantoins or N-carbamoyl-.alpha.-amino acids. Novel Coryneform bacteria were indentified and isolated based on their growth on DL-3-methyleneindolyl-5-hydantoin. One isolate, CW3, 20 g wet wt. was incubated for 24 h at 27.degree. with this substrate 80 mmol. The cell-free supernatant contained L-tryptophan 28 mmol (HPLC detn.).

FILE 'REGISTRY' ENTERED AT 10:00:11 ON 17 APR 2003

=> S N ACETYL AMINO ACID RACEMASE/CN
L10 0 N ACETYL AMINO ACID RACEMASE/CN

FILE 'CAPLUS' ENTERED AT 10:00:43 ON 17 APR 2003

=> E BOMMARIUS/AU
=> S E3-E9
1 BOMMARIUS/AU
3 "BOMMARIUS A"/AU
11 "BOMMARIUS A S"/AU
43 "BOMMARIUS ANDREAS"/AU
1 "BOMMARIUS ANDREAS DR"/AU
28 "BOMMARIUS ANDREAS S"/AU
1 "BOMMARIUS ANDREAS SEBASTIAN"/AU
L11 86 ("BOMMARIUS"/AU OR "BOMMARIUS A"/AU OR "BOMMARIUS A S"/AU OR "BOMMARIUS ANDREAS"/AU OR "BOMMARIUS ANDREAS DR"/AU OR "BOMMARIUS ANDREAS S"/AU OR "BOMMARIUS ANDREAS SEBASTIAN"/AU)

=> E DRAUZ K/AU
=> S E3-E9
16 "DRAUZ K"/AU
1 "DRAUZ KARHEINZ"/AU
12 "DRAUZ KARL HEINZ"/AU
1 "DRAUZ KARLHEIN"/AU
209 "DRAUZ KARLHEINZ"/AU
1 "DRAUZ KARLHEINZ PROF"/AU
L12 255 ("DRAUZ K"/AU OR "DRAUZ KARHEINZ"/AU OR "DRAUZ KARL HEINZ"/AU OR "DRAUZ KARLHEIN"/AU OR "DRAUZ KARLHEINZ"/AU OR "DRAUZ KARLHEI

```
                NE BRIF" AC

=> E VERSECK S/AU
=> S E3,E4
             1 "VERSECK S"/AU
             1 "VERSECK STEFAN"/AU
L11          2 "VERSECK S" AU OR "VERSECK STEFAN" AU

=> E KULA M/AU
=> S E3-E6,E7-E11
             1 "KULA M"/AU
             1 "KULA M E"/AU
           142 "KULA M R"/AU
             1 "KULA MARIA"/AU
            19 "KULA MARIA R"/AU
           148 "KULA MARIA REGINA"/AU
             1 "KULA MARIA REGINA A"/AU
L14        468 "KULA M" AU OR "KULA M E"/AU OR "KULA M R" AU OR "KULA MARIA"/A
               U OR "KULA MARIA R"/AU OR "KULA MARIA REGINA"/AU OR "KULA MARIA
               REGINA A"/AU

=> S L13,L14,L15,L16
L17          707 (L13 OR L14 OR L15 OR L16)

=> S L17 AND L5
L18            1 L17 AND L5

=> S L5 AND L17
L19            1 L5 AND L17

=> S (L18,L19) NOT (L7,L11)
L20            1 ((L18 OR L19)) NOT ((L7 OR L11))

=> D CBIB ABS

L20  ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2003 ACS
2003:19414  Document No. 138:68921  A D-hydantoinase of Arthrobacter and
      manufacture of an active form of the enzyme for use in the manufacture of
        ***N***  -  ***carbamoyl***     ***amino***     ***acids***  .
        ***Bommarius, Andreas***  ;   ***Drauz, Karlheinz***  ; May, Oliver;
      Siemann-Herzberg, Martin; Syldatk, Christoph; Werner, Markus;
      Altenbuchner, Josef (Degussa A.-G., Germany).  Eur. Pat. Appl. EP 1270730
      A2 20030102, 26 pp.  DESIGNATED STATES: R:  AT, BE, CH, DE, DK, ES, FR,
      GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL,
      TR.  (German).  CODEN: EPXXDW.  APPLICATION: EP 2002-12593 20020606.
      PRIORITY: DE 2001-10130169 20010622.
AB    A D-hydantoinase is identified in Arthrobacter crystallopoietes and
      characterized for use in the manuf. of D-amino acids from hydantoins.  The
      gene encoding the enzyme is cloned and expressed to manuf. the enzyme.
      The enzyme is recovered in active form by cultivating the bacterium in a
      medium contg. a divalent metal cation, preferably Zn2+.  The protein was
      purified 19.6-fold (14% yield) and amino acid sequence-derived degenerate
      primers used to clone the gene.  The gene (hyuP) was placed under control
      of the prior art rhamnose-regulated promoter in the expression vector
      pJOE4936.  Induction of gene expression with rhamnose increased the level
      of D-hydantoinase activity, but when the cultures contained a raised level
      of Mn2+, the activity was raised 10-fold.
```

	L #	Hits	Search Text	DBs
1	L1	2	N ADJ ACETYL ADJ AMINO ADJ ACID ADJ RACEMASE	USPAT ; US-PG PUB
2	L2	151	AMYCOLATOPSIS	USPAT ; US-PG PUB
3	L3	25	AMINO ADJ ACID ADJ RACEMASE	USPAT ; US-PG PUB
4	L5	3	L4 NOT L1	USPAT ; US-PG PUB
5	L4	5	L2 AND (L1 OR L3)	USPAT ; US-PG PUB

```
Title:          US-08-347-221-1

RESULT 2
US-08-347-221-1
; Sequence 1, Application US/08347221
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT: [illegible] et al.
;    TITLE OF INVENTION: DNA FRAGMENT ENCODING ACYLAMINO ACID
;    TITLE OF INVENTION: RACEMASE AS AMENDED
;    NUMBER OF SEQUENCES: 6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Wenderoth, Lind & Ponack
;      STREET: 805 Fifteenth Street, N.W., #700
;      CITY: Washington
;      STATE: D.C.
;      COUNTRY: U.S.A.
;      ZIP: 20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: MS-DOS
;      SOFTWARE: Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/347,221
;      FILING DATE:
;      CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 07/984,310
;      FILING DATE: December 1, 1992
;      APPLICATION NUMBER: 07/668,475
;      FILING DATE: March 13, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Warren M. Cheek Jr.
;      REGISTRATION NUMBER: 33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO: 1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1400 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
;    MOLECULE TYPE:
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
```

```
;        OTHER INFORMATION:
;      PUBLICATION INFORMATION:
;        AUTHORS:
;        TITLE:
;        JOURNAL:
;        VOLUME:
;        ISSUE:
;        PAGES:
;        DATE:
;        DOCUMENT NUMBER:
;        FILING DATE:
;        PUBLICATION DATE:
;        RELEVANT RESIDUES IN SEQ ID NO:
US-09-347-111-1

  Query Match             [illegible];  Score 863.8;  DB 1;  Length 14[illegible];
  Best Local Similarity   86.3%;  Pred. No. 1.9e-145;
  Matches  955;  Conservative    0;  Mismatches  151;  Indels    0;  Gaps    0;

Qy          1 GTGAAACTCAGCGGTGTGGAACTGCGCCGGGTCGGATGCCGCTCGTGGCCCCGTTCGGG 60

Db         61 GTGAAACTCAGCGGTGTGGAACTGCGCCGGGTGCAGATGCCGCTCGTCGGCCCGTTCGGG 121

Qy         61 ACGTCGTTCGGGACGCAGTCCGAGCGGGAATTGCTGCTGGTCCGCGCGGTGACCCCGGCG 120

Db        122 ACTTCGTTCGGCACCCAGTCGGTCCGCGAGCTCTTGCTGCTGCGCGCGGTCACGCCGGCC 181

Qy        121 GGCGAGGGCTGGGGCGAATGTGTCGCGATGGAGGCGCCGCTCTACTCGTCGGAGTACAAC 180

Db        182 GGCGAGGGCTGGGGCGAATGCGTGACGATGGCCGGTCCGCTGTACTCGTCGGAGTACAAC 241

Qy        181 GACGCCGCCGAGCACGTGCTGCGGAACCATCTGATCCCCGCACTGCTGGCGGCCGAGGAC 240

Db        242 GACGGCGCGGAACACGTGCTGCGGCACTACTTGATCCCGGCGCTGCTGGCCGCGGAAGAC 301

Qy        241 GTGACCGCGCACAAGGTGACGCCGTTGCTGGCGAAGTTCAAGGGCCACCGGATGGCGAAG 300

Db        302 ATCACCGCGGCGAAGGTGACGCCGCTGCTGGCCAAGTTCAAGGGCCACCGGATGGCCAAG 361

Qy        301 GGCGCGCTGGAGATGGCGGTCCTCGACGCCGAACTCCGCGCGCATGACCGGTCCTTCGCG 360

Db        362 GGCGCGCTGGAGATGGCCGTGCTCGACGCCGAACTCCGCGCGCACGAGAGGTCGTTCGCC 421

Qy        361 GCCGAGCTGGGGTCCACTCGCGACTCCGTGGCCTGCGGGGTCTCGGTCGGGATCATGGAC 420

Db        422 GCCGAACTCGGATCGGTGCGCGATTCTGTGCCGTGCGGCGTTTCGGTCGGGATCATGGAC 481

Qy        421 TCGATCCCGCACCTGCTCGACGTCGTCGGCGGCTACCTCGACGAGGGCTACGTCCGGATC 480

Db        482 ACCATCCCGCAACTGCTCGACGTCGTGGGCGGATACCTCGACGAGGGTTACGTGCGGATC 541

Qy        481 AAGCTGAAGATCGAGCCGGGCTGGGACGTCGAGCCGGTCCGGCAGGTGCGCGAGCGCTTC 540

Db        542 AAGCTCAAGATCGGAACCGGCTGGGACGTCGAGCCGGTGCGCGCGGTCCGCGAGCGCTTC 601

Qy        541 GGTGACGACGTGCTGCTGCAGGTCGACGCGAACACCGCGTACACGCTGGGCGACGCGCCC 600

Db        602 GGCGACGACGTGCTGCTGCAGGTCGACGCGAACACCGCCTACACCCTGGCCGACGCGCCG 661

Qy        601 CTGCTGTCCCGGCTCGACCCGTTCGACCTGCTGCTGATCGAGCAGCCGCTCGAAGAAGAG 660

Db        662 CAGCTGGCCCGGCTCGACCCGTTCGGCCTGCTGCTGATCGAGCAGCCGCTGGAAGAGGAG 721

Qy        661 GACGTGCTTGGCCACGCCGAGCTGGCCAAGCGGATCCGGACGCCGATCTGCCTCGACGAG 720

Db        722 GACGTGCTTGGCCACGCCGAACTGGCCCGCCGGATCCAGACACCGATCTGCCTCGACGAG 781

Qy        721 TCGATCGTCTCGGCCAAGGCCGCCGCGGACGCGATCAAGCTCGGCGCCTGCCAGATCGTC 780

Db        782 TCGATCGTGTCGGCCGCGGCGGCGGCGGACGCCATCAAGCTGGGCGCGGTCCAAATCGTG 841
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RESULT 1
AAF[illegible]
ID   AAF[illegible]; [illegible] AA.
XX
AC   AAF[illegible];
XX
DT   17-MAY-[illegible] (first entry
XX
DE   A. orientalis subsp lurida N-acetyl amino acid racemase protein.
XX
KW   N-acetyl amino acid racemase; AAR; enantiomerically enriched amino acid;
KW   enzyme-membrane reactor; N-acetyl-D-methionine; N-acetyl-L-methionine;
KW   L-methionine; heavy metal dependency.
XX
OS   Amycolatopsis orientalis.
XX
PN   EP1074608-A1.
XX
PD   07-FEB-2001.
XX
PF   03-JUL-2000; 2000EP-1116912.
XX
PR   [illegible]-JUL-1999; 99DE-1[illegible]d8.
XX
PA   (DEGS) DEGUSSA-HUELS AG.
XX
PI   Verseck S, Kula M, Bommarius A, Draus W;
XX
DR   WPI; 2001-161182/17.
DR   N-PSDB; AAF61120.
XX
PT   New N-acetyl amino acid racemase enzyme derived from Amycolatopsis
PT   orientalis ssp. lurida, useful for producing enantiomerically enriched
PT   amino acids -
XX
PS   Disclosure; Page 10-13; 23pp; German.
XX
CC   This invention describes a novel N-acetyl amino acid racemase (AAR)
CC   enzyme (I) derived from Amycolatopsis orientalis ssp. lurida (DSM 43134).
CC   The invention also describes (1) a gene coding for (I); (2) a vector
CC   containing the gene; (3) a microorganism containing the gene; (4) a
CC   primer for the gene; and (5) a probe for the gene. (I) is useful for
CC   producing enantiomerically enriched amino acids in an enzyme-membrane
CC   reactor, e.g. by AAR-catalysed conversion of N-acetyl-D-methionine to
CC   N-acetyl-L-methionine followed by acylase-catalysed conversion to
CC   L-methionine. (I) exhibits reduced heavy metal dependency compared with
CC   the AAR of Amycolatopsis sp. TS-1-6 (Appl. Microbiol. Biotechnol., 42,
CC   853, 1995).
XX
SQ   Sequence 360 AA;

  Query Match   [illegible] ; Score 1898; DB 22; Length 360;
  Best Local Similarity   [illegible]%; Pred. No. 1.4e-181;
  Matches 360; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MKLSGVELRRVRMPLVAPFRTSFGTQSERELLLVRAVTPAGEGWGECVAMEAPLYSSEYN 60

Db   1 MKLSGVELRRVRMPLVAPFRTSFGTQSERELLLVRAVTPAGEGWGECVAMEAPLYSSEYN 60

Qy   61 DAAEHVLRNHLIPALLAAEDVTAHKVTPLLAKFKGHRMAKGALEMAVLDAELRAHDRSFA 120

Db   61 DAAEHVLRNHLIPALLAAEDVTAHKVTPLLAKFKGHRMAKGALEMAVLDAELRAHDRSFA 120

Qy   121 AELGSTRDSVACGVSVGIMDSIPHLLDVTGGYLDEGYVRIKLKIEPGWDVEPVRQVRERF 180

Db   121 AELGSTRDSVACGVSVGIMDSIPHLLDVTGGYLDEGYVRIKLKIEPGWDVEPVRQVRERF 180

Qy   181 GDDVLLQVDANTAYTLGDAPLLSRLDPFDLLLIEQPLEEEDVLGHAELAKRIRTPICLDE 240

```
Title: [illegible]

RESULT 1
[illegible]
N-Acylamino acid racemase - Amycolatopsis sp.
C;Species: Amycolatopsis sp.
C;Date: [illegible]
C;Accession: [illegible]
R;Tokuyama, S.; Hatano, K.
Appl. Microbiol. Biotechnol. 42, 884-889, 1995
A;Title: Cloning, DNA sequencing and heterologous expression of the gene for thermostable n-acylamino acid racemase from amycolatopsis sp. ts-1-60 in escherichia coli.
A;Reference number: [illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: [illegible]
A;Status: preliminary; translated from GB EMBL DDBJ
A;Molecule type: DNA
A;Residues: 1-368 &lt;RES&gt;
A;Cross-references: GB:[illegible]; NID:[illegible]; PIDN:BAA[illegible].1; PID:[illegible]
C;Genetics:
A;Gene: aaaR
A;Start codon: GTG
C;Superfamily: muconate cycloisomerase

  Query Match             91.8%;  Score 1719;  DB 1;  Length 368;
  Best Local Similarity   90.5%;  Pred. No. 4.4e-120;
  Matches  333;  Conservative   14;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 VKLSGVELRRVRMPLVAPFRTSFGTQSERELLLVRAVTPAGEGWGECVAMEAPLYSSEYN 60

Db          1 MKLSGVELRRVQMPLVAPFRTSFGTQSVRELLLLRAVTPAGEGWGECVTMAGPLYSSEYN 60

Qy         61 DAAEHVLRNHLIPALLAAEDVTAHKVTPLLAKFKGHRMAKGALEMAVLDAELRAHDRSFA 120

Db         61 DGAEHVLRHYLIPALLAAEDITAAKVTPLLAKFKGHRMAKGALEMAVLDAELRAHERSFA 120

Qy        121 AELGSTRDSVACGVSVGIMDSIPHLLDVVGGYLDEGYVRIKLKIEPGWDVEPVRQVRERF 180

Db        121 AELGSVRDSVPCGVSVGIMDTIPQLLDVVGGYLDEGYVRIKLKIEPGWDVEPVRAVRERF 180

Qy        181 GDDVLLQVDANTAYTLGDAPLLSRLDPFDLLLIEQPLEEEDVLGHAELAKRIRTPICLDE 240

Db        181 GDDVLLQVDANTAYTLGDAPQLARLDPFGLLLIEQPLEEEDVLGHAELARRIQTPICLDE 240

Qy        241 SIVSAKAAADAIKLGACQIVNIKPGRVGGYLEARRVHDVCAAHGIAVWCGGMIETGLGRA 300

Db        241 SIVSARAAADAIKLGAVQIVNIKPGRVGGYLEARRVHDVCAAHGIPVWCGGMIETGLGRA 300

Qy        301 ANVALASLPGFTLPGDTSASGRFYRTDITEPFVLDAGHLPVPTGPGLGVTPIPDLLDEVT 360

Db        301 ANVALASLPNFTLPGDTSASDRFYKTDITEPFVLSGGHLPVPTGPGLGVAPIPELLDEVT 360

Qy        361 TEKAWIGS 368

Db        361 TAKVWIGS 368
```